(FILE 'HOME' ENTERED AT 13:07:47 ON 06 MAR 2001)

FILE 'CAPLUS, USPATFULL' ENTERED AT 13:07:55 ON 06 MAR 2001

L1	0	S	COMPETITIVE PROBE HYBRIDIZATION
L2	1326	S	COMPET? (P) PROBE (P)HYBRID?
L3	274	S	COMPET? (5A) PROBE (5A)HYBRID?
L4	274		DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)
L5	8	S	L4 AND (OPTIMIZ? (P) TEMPERATURE)

L5 ANSWER 2 OF 8 USPATFULL

SUMM . . . exogenous DNA (e.g., DNA spilled onto lab surfaces) or cross-contamination is also a major consideration. Reaction conditions must be carefully **optimized** for each different primer pair and target sequence, and the process can take days, even for an experienced investigator. The. . . to penetrate the clinical market in a significant way. The same concerns arise with LCR, as LCR must also be **optimized** to use different oligonucleotide sequences for each target sequence. In addition, both methods require expensive equipment, capable of precise **temperature** cycling.

DETD . . . contains sequences at its 3' end which are substantially the same as sequences located at the 5' end of a **probe** oligonucleotide; these regions will **compete** for **hybridization** to the same segment along a complementary target nucleic acid.

DETD **Temperature** is also an important factor in the hybridization of oligonucleotides. The range of **temperature** tested will depend in large part, on the design of the oligonucleotides, as discussed above. In a preferred embodiment, the. . . a nucleic acid is only an approximation, the reaction temperatures chosen for initial tests should bracket the calculated T.sub.m. While **optimizations** are not limited to this, 5.degree. C. increments are convenient test intervals in these **optimization** assays.

DETD . . . manufacturer's instructions are a resource for this information. When developing an assay utilizing any particular cleavage agent, the oligonucleotide and **temperature** **optimizations** described above should be performed in the buffer conditions best suited to that cleavage agent.

DETD . . . by the addition of 5 .mu.l of the appropriate enzyme mixture. The reaction mixtures were then incubated at 63.degree. C. **temperature** for 15 minutes. The reactions were stopped by the addition of 8 .mu.l of 95% formamide with 20 mM EDTA. . . nucleases tested have the ability to catalyze invader-directed cleavage in at least one of the buffer systems tested. Although not **optimized** here, these cleavage agents are suitable for use in the methods of the present invention.

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L5 ANSWER 2 OF 8 USPATFULL

AN 2000:91698 USPATFULL

TI Cleavage of nucleic acids

IN Prudent, James R., Madison, WI, United States
Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
Dahlberg, James E., Madison, WI, United States

PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)

PI US 6090543 20000718

AI US 1996-759038 19961202 (8)

RLI Continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996 which is a continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996 which is a continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996 76 Ser. No. US 1996-758314, filed on 2 Dec 1996

DT Utility
EXNAM Primary Examin[redacted] Jones, W. Gary; Assistant Exa[redacted]er: Shoemaker, Debra
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 102 Drawing Figure(s); 117 Drawing Page(s)
LN.CNT 11426
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of nucleic acid sequences, as well as variations in nucleic acid sequences. The present invention also relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving the nucleic acid cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof.

L5 ANSWER 3 OF 8 USPATFULL
AN 1999:163423 USPATFULL
TI Detection of nucleic acid sequences by invader-directed cleavage
IN Brow, Mary Ann D., Madison, WI, United States
Hall, Jeff Steven Groteluesch en, Madison, WI, United States
Lyamichev, Victor, Madison, WI, United States
Olive, David Michael, Madison, WI, United States
Prudent, James Robert, Madison, WI, United States
PA Third Wave Technologies, Inc., CA, United States (U.S. corporation)
PI US 6001567 19991214
AI US 1996-682853 19960712 (8)
RLI Continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717
DT Utility
EXNAM Primary Examiner: Arthur, Lisa B.; Assistant Examiner: Souaya, Jehanne
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 66 Drawing Figure(s); 82 Drawing Page(s)
LN.CNT 7836
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of nucleic acid sequences, as well as variations in nucleic acid sequences. The present invention also relates to methods for forming a nucleic acid cleavage structure on a target sequence and cleaving the nucleic acid cleavage structure in a site-specific manner. The 5' nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific nucleic acid sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of nucleic acid molecules based by charge.

L5 ANSWER 7 OF 8 USPATFULL
AN 88:53750 USPATFULL
TI Displacement polynucleotide assay employing polyether and diagnostic kit
IN Williams, Jon I., Montclair, NJ, United States
Ellwood, Marian S., Summit, NJ, United States
Collins, Mary, Natick, MA, United States
Fritsch, Edward F., Concord, MA, United States
Brewen, Joseph G., Convent Station, NJ, United States
Diamond, Steven E., Springfield, NJ, United States
PA Allied Corporation, Morristown, NJ, United States (U.S. corporation)
Genetics Institute, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 4766064 19880823
AI US 1984-684308 19841220 (6)
DCD 20010529
RLI Continuation-in-part of Ser. No. US 1984-607885, filed on 7 May 1984
DT Utility
EXNAM Primary Examiner: Warren, Charles F.; Assistant Examiner: Jay, Jeremy M.
LREP Doernberg, Alan M.
CLMN Number of Claims: 31
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 1834
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A diagnostic reagent is disclosed containing a complex of a probe polynucleotide (P) bound via purine/pyrimidine hydrogen bonding to a labeled polynucleotide (L). The probe (P) contains a target binding region (TBR) capable of binding to a target nucleotide sequence (G) of a biological sample. A method is disclosed in which contact with a sample containing the target nucleotide sequence (G) causes binding, initially between G and a single-stranded portion (IBR) of the target binding region (TBR). Thereafter the labeled polynucleotide (L) is displaced from the complex by branch migration of (G) into the (P)/(L) binding region. A volume excluding polymeric agent such as poly(ethylene oxide) (PEO or PEG) or other polyethers enhances the rate of appearance of displaced labeled polynucleotide. Determination of displaced labeled polynucleotide (L) gives a value which is a function of the presence and concentration of target nucleotide sequence (G) in the sample.

L6 ANSWER 1 OF 1 USPATFULL
AN 1998:22060 USPATFULL
TI Amplification and detection of mycobacterial DNA K nucleic acids
IN Nycz, Colleen Marie, Raleigh, NC, United States
Nadeau, James G., Chapel Hill, NC, United States
Scott, Patricia Brinkley, Apex, NC, United States
Shank, Daryl Dee, BelAir, MD, United States
Spears, Patricia Anne, Raleigh, NC, United States
PA Becton, Dickinson and Company, Franklin Lakes, NJ, United States (U.S. corporation)
PI US 5723296 19980303
AI US 1996-644729 19960510 (8)
RLI Continuation of Ser. No. US 1994-347551, filed on 30 Nov 1994, now abandoned
DT Utility
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Fredman, Jeffrey
LREP Fugit, Donna R.
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 1269
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods for identification or detection of a species of an organism or a group of related species of an organism by species non-specific amplification of a target sequence followed by species- or group-specific detection of the amplification products. Also provided are a target sequence which is amplifiable in multiple species of mycobacteria using a single pair of amplification primers and species- and group-specific detector probes for hybridization to the assay regioin of the amplified target. Blocking oligonucleotides are employed to allow discrimination among species in which the amplified target sequences are sufficiently similar that they cross-hybridize to an assay probe.

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L6 ANSWER 1 OF 1 USPATFULL
DETD . . . temperatures resulted in equivalent or higher signal from M. avium and M. intracellulare, but also increased signal from M. chelonae.
Temperature optimization for assay **hybridization** using the blocker **probe** SEQ ID NO: 11 indicated that 42.5.degree. C. hybridization gave the best ratio of specific- to non-specific signal and provided >100 fold discrimination between signals from the specific and non-specific targets. Such hybridization **temperature** studies are routine for **optimizing hybridization** of a **probe** or primer to its target sequence and would usually be performed to optimize the performance of any blocking oligonucleotide.